



UNIVERSITÀ
DEGLI STUDI
FIRENZE

FLORE

Repository istituzionale dell'Università degli Studi di Firenze

Integrative proteomics: prespective in complex system interpretation

Questa è la Versione finale referata (Post print/Accepted manuscript) della seguente pubblicazione:

Original Citation:

Integrative proteomics: prespective in complex system interpretation / A. Urbani; A. Modesti; A.M. Timperio; L. Bini; M. Castagnola; m. Fasano; P. Roncada. - In: MOLECULAR BIOSYSTEMS. - ISSN 1742-2051. - ELETTRONICO. - 8:(2012), pp. 951-952.

Availability:

The webpage <https://hdl.handle.net/2158/650623> of the repository was last updated on 2021-02-08T16:08:54Z

Terms of use:

Open Access

La pubblicazione è resa disponibile sotto le norme e i termini della licenza di deposito, secondo quanto stabilito dalla Policy per l'accesso aperto dell'Università degli Studi di Firenze (<https://www.sba.unifi.it/upload/policy-oa-2016-1.pdf>)

Publisher copyright claim:

La data sopra indicata si riferisce all'ultimo aggiornamento della scheda del Repository FloRe - The above-mentioned date refers to the last update of the record in the Institutional Repository FloRe

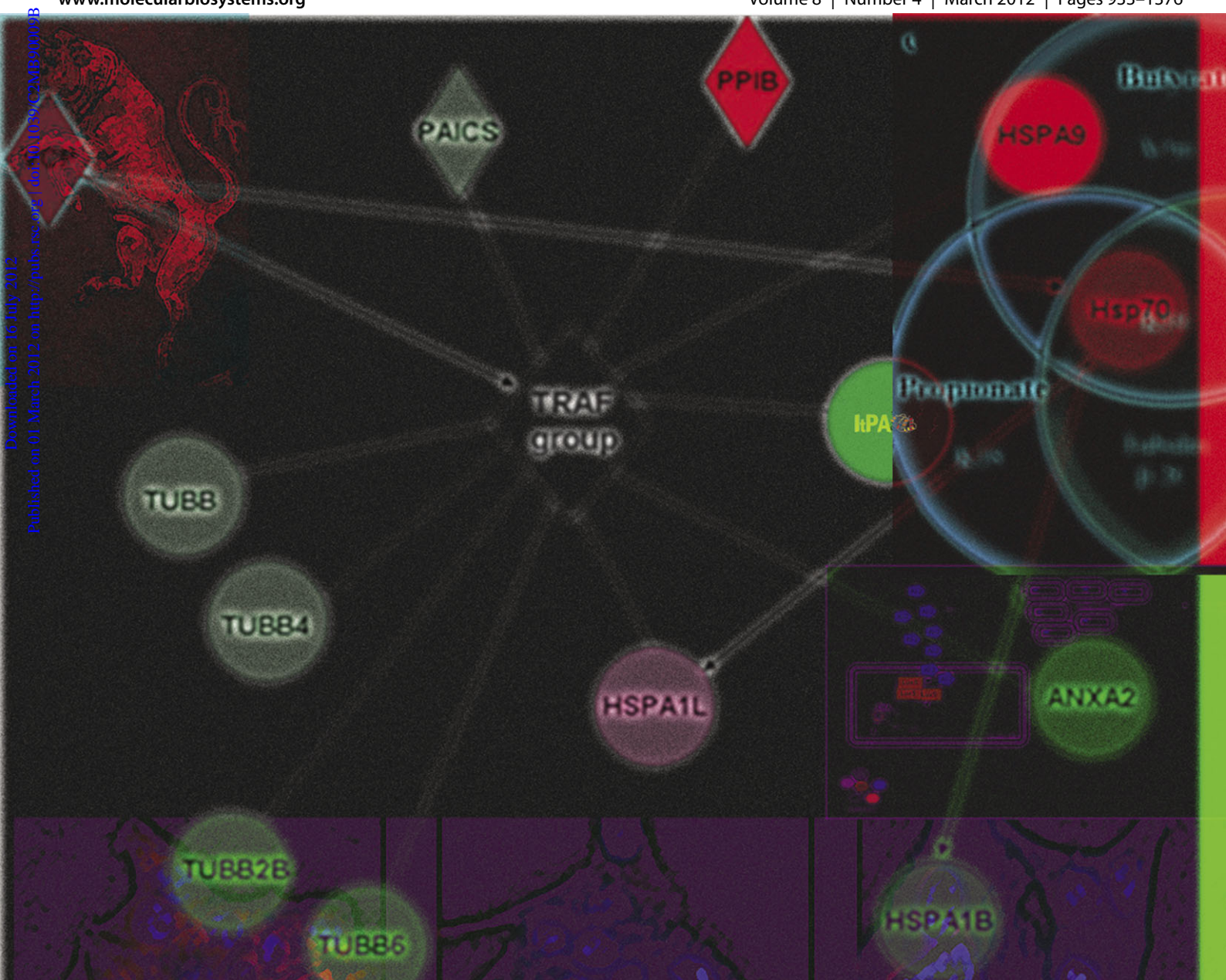
(Article begins on next page)

Indexed in
MEDLINE!

Molecular BioSystems

www.molecularbiosystems.org

Volume 8 | Number 4 | March 2012 | Pages 933–1376



Downloaded on 16 July 2012
Published on 01 March 2012 on http://pubs.rsc.org | doi:10.1039/C2MB90009B

Themed issue: Italian Proteomics Association

ISSN 1742-206X

RSC Publishing

EDITORIAL

Andrea Urbani *et al.*

Directory Board of the Italian Proteomics Association (www.itpa.it) introduce this *Molecular BioSystems* themed issue on proteomics.



1742-206X(2012)8:4;1-9

Integrative proteomics: perspective in complex system interpretation

Andrea Urbani,^{*ab} Alessandra Modesti,^c Anna Maria Timperio,^d Luca Bini,^e
Massimo Castagnola,^{fg} Mauro Fasano^h and Paola Roncadaⁱ

DOI: 10.1039/c2mb90009b

In the development of new integrative molecular models of living organisms, proteomics investigations are becoming a key dataset. The hidden relationships between molecular effectors of specific biochemical phenomena are often explored by profiling the relative distribution of proteins levels, which may act as a molecular remnant of a defined mechanism. Proteome investigations often suffer from a limited in depth analysis of primary switch molecules such as the receptor tyrosine kinases whose proteomics investigations are deeply reviewed by Dr P. Huang (DOI: 10.1039/c1mb05327b). This is due to the bias we obtain in the evaluation of abundant proteins which may mask the direct analysis of low concentration regulatory polypeptides. This scenario is clearly observed when a network of ontological relationships is developed for the identified proteins in an open differential proteomics profile, where the experimentally mapped proteins in open proteomics profiling mostly lie on

the periphery of such a relationship graph. The centre of the network is therefore computationally associated to molecular partners which have multiple interactions with the experimentally covered protein. This distribution is clearly visible in a number of papers in this themed issue on proteomics, following the Italian Proteomics Association's (www.itpa.it) National Congress in Turin (21st–24th June 2011).

The reported ontological network analyses have been clearly informative over the primary effector molecules. The paper from D. Pieragostino *et al.* (DOI: 10.1039/c1mb05357d) shows such a distribution following an investigation into the tears of patients with Primary open angle (POAG) and pseudoexfoliative glaucoma (PXG), which are the most common primary and secondary forms of glaucoma. The paper from F. Raimondo *et al.* (DOI: 10.1039/c2mb05390j) applies a functional protein network analysis to highlight the fundamental characteristics of renal cell carcinoma. Such an integrative evaluation, always on a clinical proteomics study, has been proposed by L. Giusti *et al.* (DOI: 10.1039/c2mb05394b) where the washing fluids of colon tract resection form patients with different stages of colon-rectal carcinoma have been investigated. Nevertheless, such complex data interpretation needs to be experimentally validated. The network analysis proposed by A. Sau *et al.* (DOI: 10.1039/c1mb05295k) provides key evidence on the potential mechanism of a new anti-cancer compound, NBDHEX, in treating osteosarcoma. The overall proteomics investigation coupled to functional network analysis provided key evidence for the identification of the

TRAF2–GST P1 interaction mechanism in the action of this promising molecule. This paper experimentally demonstrates the results obtained from the ontological analysis. Such an experimental validation of a complex network analysis of nanoLC shotgun proteomics analysis has been successfully pursued in the paper from S. D'Aguzzo *et al.* (DOI: 10.1039/c2mb05498a), where the involvement of nrf2 in response to curcumin in neuroblastoma cell models has been deduced by bioinformatic analysis and afterwards experimentally validated.

The bioinformatics repositories of functional relationships are biased toward human, mouse and rat data, due to the large campaigns of data collection which have been pursued in the last decade following biomedical research. Investigating other species is often complicated by the lack of appropriate bioinformatic tools and requires specific personal expertise. This is the case in the paper from C. Piras *et al.* (DOI: 10.1039/c1mb05385j) where the complex world of *E. Coli* sub-strains following phenotypic selection over multi-drug resistance biological pressure is investigated by state of the art proteomics tools. Therefore, following an integrative vision of biological systems investigation, it is also desirable to find correlations related to nucleic acid and metabolite profiles. The latter of which still requires the development of specific sensitive tools in order to tackle significant biological samples. In this light, the paper of A. D'Alessandro *et al.* (DOI: 10.1039/c1mb05358b) describes an important technological development for metabonomics investigation from blastocele fluids.

^a Department of Internal Medicine, University of Rome "Tor Vergata", Rome. Fax: +39-06-501703332;

E-mail: andrea.urbani@uniroma2.it

^b IRCCS-Fondazione S. Lucia, Rome

^c Department of Biochemical Sciences, University of Florence, Italy

^d Dipartimento di Scienze Ambientali, Università della Tuscia, Viterbo

^e Department of Biotechnologies, University of Siena, Italy

^f Istituto di Biochimica e di Biochimica Clinica, Università Cattolica, Rome

^g Istituto di Chimica del Riconoscimento Molecolare, CNR, Rome

^h Department of Theoretical and Applied Sciences, and Center of Neuroscience, University of Insubria, Busto Arsizio

ⁱ Section of Proteomics, Istituto Sperimentale Italiano L. Spallanzani, University of Milano, Milano, Italy

In the end, we may consider the protein profile as a remnant of the molecular hallmarks of the biological and biochemical phenomena. As the Turin Shroud bears the image of Christ, the protein ontological network analysis

bears the image of the key effectors of the biological system under investigation. Nevertheless, proteomics are always visible and open to direct experimental evaluation by scientists, unlike the Turin Shroud.

It is our hope that this series of themed issue papers will provide a new scenario towards integrative research in biochemistry, providing a novel framework for large international initiatives such as the Human Proteome Project.